

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/910,185

DATE: 08/02/2001

TIME: 10:56:08

Input Set : A:\RTS-0258 Sequence Listing.txt

Output Set: N:\CRF3\08022001\I910185.raw

6 <110> APPLICANT: C. Frank Bennett

7 Susan M. Freier

9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-3

EXPRESSION

11 <130> FILE REFERENCE: RTS-0258

C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/910,185

C--> 13 <141> CURRENT FILING DATE: 2001-07-18

13 <160> NUMBER OF SEQ ID NOS: 90

16 <210> SEQ ID NO: 1

17 <211> LENGTH: 20

18 <212> TYPE: DNA

19 <213> ORGANISM: Artificial Sequence

21 <220> FEATURE:

23 <223> OTHER INFORMATION: Antisense Oligonucleotide

25 <400> SEQUENCE: 1

26 tccgtcatcg ctctcaggg

20

29 <210> SEQ ID NO: 2

30 <211> LENGTH: 20

31 <212> TYPE: DNA

32 <213> ORGANISM: Artificial Sequence

34 <220> FEATURE:

36 <223> OTHER INFORMATION: Antisense Oligonucleotide

38 <400> SEQUENCE: 2

20

39 atgcattctg cccccaagga

42 <210> SEQ ID NO: 3

43 <211> LENGTH: 5055

44 <212> TYPE: DNA

45 <213> ORGANISM: Homo sapiens

47 <220> FEATURE:

49 <220> FEATURE:

50 <221> NAME/KEY: CDS

51 <222> LOCATION: (55)...(4845)

53 <400> SEQUENCE: 3

54 cgatactacg tgggcatttt tggtcgaaga gagctgaagt aatgagaaga catc atg

57

55 Met

56 1

58 gag gcc cag tcc cac agc tcc acg acc act gaa aag aaa aaa gtt gag

105

59 Glu Ala Gln Ser His Ser Ser Thr Thr Glu Lys Lys Lys Val Glu

60 5 10 15

62 aat tcc ata gtg aag tgc tcc act cga aca gat gtg agc gag aaa gcc

153

63 Asn Ser Ile Val Lys Cys Ser Thr Arg Thr Asp Val Ser Glu Lys Ala

64 20 25 30

66 gtt gcc tcc agc acc act tct aat gag gat gaa agt cct gga cag act

201

67 Val Ala Ser Ser Thr Thr Ser Asn Glu Asp Glu Ser Pro Gly Gln Thr

68 35 40 45

70 tat cac aga gag aga aga aac gca atc act atg cag cca cag aat gtc

249

71 Tyr His Arg Glu Arg Arg Asn Ala Ile Thr Met Gln Pro Gln Asn Val

72 50 55 60 65

Does Not Comply
Corrected Diskette Needed

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74	cag ggg ctc agc aaa gtc agt gag gaa cct tca aca tcg agt gac gag	297
75	Gln Gly Leu Ser Lys Val Ser Glu Glu Pro Ser Thr Ser Ser Asp Glu	
76	70 75 80	
78	agg gcc tca ttg atc aag aaa gag atc cat ggg tcc ctg cca cac gtg	345
79	Arg Ala Ser Leu Ile Lys Lys Glu Ile His Gly Ser Leu Pro His Val	
80	85 90 95	
82	gcg gag ccc tct gtg ccg tac cgc ggg acg gtg ttt gcc atg gac ccc	393
83	Ala Glu Pro Ser Val Pro Tyr Arg Gly Thr Val Phe Ala Met Asp Pro	
84	100 105 110	
86	agg aat ggt tac atg gag ccc cac tac cac cct cct cat ctt ttc cct	441
87	Arg Asn Gly Tyr Met Glu Pro His Tyr His Pro Pro His Leu Phe Pro	
88	115 120 125	
90	gcc ttc cat cct cct gta cca att gat gcc aga cat cat gag ggc cgt	489
91	Ala Phe His Pro Pro Val Pro Ile Asp Ala Arg His His Glu Gly Arg	
92	130 135 140 145	
94	tac cat tac gat cca tct ccg att cct cca ttg cat atg act tcc gcc	537
95	Tyr His Tyr Asp Pro Ser Pro Ile Pro Pro Leu His Met Thr Ser Ala	
96	150 155 160	
98	tta tct agt agc cct acg tat ccg gac ctg ccc ttc att agg atc tcc	585
99	Leu Ser Ser Ser Pro Thr Tyr Pro Asp Leu Pro Phe Ile Arg Ile Ser	
100	165 170 175	
102	cca cac cgg aac ccc gct gct gct tcc gag tct ccc ttc agc cct cca	633
103	Pro His Arg Asn Pro Ala Ala Ala Ser Glu Ser Pro Phe Ser Pro Pro	
104	180 185 190	
106	cat ccc tac att aat ccc tac atg gac tat atc cgc tcc ttg cac agc	681
107	His Pro Tyr Ile Asn Pro Tyr Met Asp Tyr Ile Arg Ser Leu His Ser	
108	195 200 205	
110	agc cca tcg ctc tcc atg atc tca gca acc cgt ggg ctg agc cct aca	729
111	Ser Pro Ser Leu Ser Met Ile Ser Ala Thr Arg Gly Leu Ser Pro Thr	
112	210 215 220 225	
114	gat gcg ccc cat gca gga gtc agc cca gca gaa tac tat cat cag atg	777
115	Asp Ala Pro His Ala Gly Val Ser Pro Ala Glu Tyr Tyr His Gln Met	
116	230 235 240	
118	gcc ctg cta act ggc cag cgc agc ccc tat gca gac att att ccc tca	825
119	Ala Leu Leu Thr Gly Gln Arg Ser Pro Tyr Ala Asp Ile Ile Pro Ser	
120	245 250 255	
122	gct gcc acc gcc ggc acg ggg gcc atc cac atg gaa tat ctt cat gct	873
123	Ala Ala Thr Ala Gly Thr Gly Ala Ile His Met Glu Tyr Leu His Ala	
124	260 265 270	
126	atg gat agc acc aga ttc tcc agc ccc agg ctg tca gcc agg ccg agc	921
127	Met Asp Ser Thr Arg Phe Ser Ser Pro Arg Leu Ser Ala Arg Pro Ser	
128	275 280 285	
130	cga aaa cgt aca ctg tcc ata tca cca ctc tcc gat cat agc ttt gac	969
131	Arg Lys Arg Thr Leu Ser Ile Ser Pro Leu Ser Asp His Ser Phe Asp	
132	290 295 300 305	
134	ctt cag acc atg ata agg acg tct ccc aac tcc ttg gtc acg att ctc	1017
135	Leu Gln Thr Met Ile Arg Thr Ser Pro Asn Ser Leu Val Thr Ile Leu	
136	310 315 320	
138	aat aat tcc cgt agc agc tct tca gca agt ggc tcc tat ggt cac tta	1065

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139	Asn	Asn	Ser	Arg	Ser	Ser	Ser	Ser	Ala	Ser	Gly	Ser	Tyr	Gly	His	Leu	
140				325					330					335			
142	tct	gca	agt	gca	atc	agc	cct	gcc	ttg	agc	ttc	acc	tac	tct	tcc	gcg	1113
143	Ser	Ala	Ser	Ala	Ile	Ser	Pro	Ala	Leu	Ser	Phe	Thr	Tyr	Ser	Ser	Ala	
144			340					345					350				
146	ccc	gtc	tct	ctc	cac	atg	cat	cag	cag	atc	cta	agc	cga	caa	cag	agc	1161
147	Pro	Val	Ser	Leu	His	Met	His	Gln	Gln	Ile	Leu	Ser	Arg	Gln	Gln	Ser	
148		355					360					365					
150	tta	ggt	tca	gcc	ttt	gga	cac	agc	cct	cca	ctc	atc	cac	cct	gcc	cca	1209
151	Leu	Gly	Ser	Ala	Phe	Gly	His	Ser	Pro	Pro	Leu	Ile	His	Pro	Ala	Pro	
152	370					375					380					385	
154	act	ttt	cca	aca	cag	agg	cct	att	cca	ggg	atc	cct	acg	gtt	ctg	aac	1257
155	Thr	Phe	Pro	Thr	Gln	Arg	Pro	Ile	Pro	Gly	Ile	Pro	Thr	Val	Leu	Asn	
156				390					395					400			
158	ccc	gtc	cag	gtc	agc	tcc	ggc	cct	tct	gag	tcc	tca	cag	aac	aag	ccc	1305
159	Pro	Val	Gln	Val	Ser	Ser	Gly	Pro	Ser	Glu	Ser	Ser	Gln	Asn	Lys	Pro	
160			405					410					415				
162	acg	agt	gag	tct	gca	gtg	agc	agc	act	ggt	gac	ccg	atg	cac	aac	aag	1353
163	Thr	Ser	Glu	Ser	Ala	Val	Ser	Ser	Thr	Gly	Asp	Pro	Met	His	Asn	Lys	
164		420					425					430					
166	agg	tcc	aag	atc	aaa	ccc	gat	gaa	gac	ctc	ccc	agc	cca	ggg	gct	cgg	1401
167	Arg	Ser	Lys	Ile	Lys	Pro	Asp	Glu	Asp	Leu	Pro	Ser	Pro	Gly	Ala	Arg	
168		435				440					445						
170	ggg	cag	cag	gaa	cag	ccc	gaa	gga	aca	acc	ctt	gtc	aag	gag	gaa	ggg	1449
171	Gly	Gln	Gln	Glu	Gln	Pro	Glu	Gly	Thr	Thr	Leu	Val	Lys	Glu	Glu	Gly	
172	450				455					460					465		
174	gac	aaa	gat	gaa	agc	aaa	cag	gag	cct	gaa	gtc	atc	tat	gag	aca	aac	1497
175	Asp	Lys	Asp	Glu	Ser	Lys	Gln	Glu	Pro	Glu	Val	Ile	Tyr	Glu	Thr	Asn	
176			470					475					480				
178	tgc	cac	tgg	gaa	ggc	tgc	gcg	agg	gag	ttc	gac	acc	caa	gag	cag	ctt	1545
179	Cys	His	Trp	Glu	Gly	Cys	Ala	Arg	Glu	Phe	Asp	Thr	Gln	Glu	Gln	Leu	
180			485				490					495					
182	gtg	cac	cat	ata	aat	aac	gac	cat	att	cat	gga	gag	aag	aag	gag	ttc	1593
183	Val	His	His	Ile	Asn	Asn	Asp	His	Ile	His	Gly	Glu	Lys	Lys	Glu	Phe	
184		500				505						510					
186	gtg	tgc	agg	tgg	ctg	gac	tgc	tca	aga	gag	cag	aaa	ccc	ttc	aaa	gcc	1641
187	Val	Cys	Arg	Trp	Leu	Asp	Cys	Ser	Arg	Glu	Gln	Lys	Pro	Phe	Lys	Ala	
188		515				520					525						
190	cag	tat	atg	ttg	gta	gtg	cat	atg	aga	aga	cac	acg	ggc	gag	aag	cct	1689
191	Gln	Tyr	Met	Leu	Val	Val	His	Met	Arg	Arg	His	Thr	Gly	Glu	Lys	Pro	
192	530				535					540					545		
194	cac	aaa	tgc	act	ttt	gaa	ggt	tgc	aca	aag	gcc	tac	tcg	aga	cta	gaa	1737
195	His	Lys	Cys	Thr	Phe	Glu	Gly	Cys	Thr	Lys	Ala	Tyr	Ser	Arg	Leu	Glu	
196				550				555				560					
198	aac	ttg	aaa	aca	cac	ttg	aga	tct	cac	act	gga	gag	aaa	cca	tac	gtc	1785
199	Asn	Leu	Lys	Thr	His	Leu	Arg	Ser	His	Thr	Gly	Glu	Lys	Pro	Tyr	Val	
200			565				570					575					
202	tgt	gag	cac	gaa	ggt	tgc	aac	aag	gct	ttc	tca	aat	gcc	tct	gat	cgc	1833
203	Cys	Glu	His	Glu	Gly	Cys	Asn	Lys	Ala	Phe	Ser	Asn	Ala	Ser	Asp	Arg	

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204	580	585	590	1881
206	gcc aaa cac caa aac aga acg cat tcc aat gag aaa cca tat gtg tgc			
207	Ala Lys His Gln Asn Arg Thr His Ser Asn Glu Lys Pro Tyr Val Cys			
208	595	600	605	1929
210	aaa atc cca ggc tgc act aag cgt tac aca gac cca agc tcc ctc cgg			
211	Lys Ile Pro Gly Cys Thr Lys Arg Tyr Thr Asp Pro Ser Ser Leu Arg			
212	610	615	620	1977
214	aaa cat gtg aag aca gtg cat ggc cca gag gct cat gtc acc aag aag			
215	Lys His Val Lys Thr Val His Gly Pro Glu Ala His Val Thr Lys Lys			
216	630	635	640	2025
218	cag cga ggg gac atc cat cct cgg ccg cca ccc ccg aga gat tcc ggc			
219	Gln Arg Gly Asp Ile His Pro Arg Pro Pro Pro Pro Arg Asp Ser Gly			
220	645	650	655	2073
222	agc cat tca cag tcc agg tcg cct ggc cga ccg act cag gga gcc ctt			
223	Ser His Ser Gln Ser Arg Ser Pro Gly Arg Pro Thr Gln Gly Ala Leu			
224	660	665	670	2121
226	ggt gag cag cag gac ctc agc aac act acc tca aag cgg gaa gaa tgc			
227	Gly Glu Gln Gln Asp Leu Ser Asn Thr Thr Ser Lys Arg Glu Glu Cys			
228	675	680	685	2169
230	ctc cag gtg aaa acc gtc aag gca gag aag cca atg aca tct cag cca			
231	Leu Gln Val Lys Thr Val Lys Ala Glu Lys Pro Met Thr Ser Gln Pro			
232	690	695	700	2217
234	agc cct ggt ggt cag tct tca tgc agc agc caa cag tcc ccc atc agc			
235	Ser Pro Gly Gly Gln Ser Ser Cys Ser Ser Gln Gln Ser Pro Ile Ser			
236	710	715	720	2265
238	aac tat tcc aac agt ggg ctc gag ctt cct ctg acc gat gga ggt agt			
239	Asn Tyr Ser Asn Ser Gly Leu Glu Leu Pro Leu Thr Asp Gly Gly Ser			
240	725	730	735	2313
242	ata gga gac ctc agt gcc atc gat gaa acc cca atc atg gac tca acc			
243	Ile Gly Asp Leu Ser Ala Ile Asp Glu Thr Pro Ile Met Asp Ser Thr			
244	740	745	750	2361
246	att tcc act gca acc aca gcc ctt gct ttg caa gcc agg aga aac ccg			
247	Ile Ser Thr Ala Thr Thr Ala Leu Ala Leu Gln Ala Arg Arg Asn Pro			
248	755	760	765	2409
250	gca ggg acc aaa tgg atg gag cac gta aaa cta gaa agg cta aaa caa			
251	Ala Gly Thr Lys Trp Met Glu His Val Lys Leu Glu Arg Leu Lys Gln			
252	770	775	780	2457
254	gtg aat gga atg ttt ccg cga ctg aac ccc att cta ccc cct aaa gcc			
255	Val Asn Gly Met Phe Pro Arg Leu Asn Pro Ile Leu Pro Pro Lys Ala			
256	790	795	800	2505
258	cct gcg gtc tct cct ctc ata gga aat ggc aca cag tcc aac aac acc			
259	Pro Ala Val Ser Pro Leu Ile Gly Asn Gly Thr Gln Ser Asn Asn Thr			
260	805	810	815	2553
262	tgc agc ttg ggt ggg ccc atg acg ctt ctc ccg ggc aga agc gac ctc			
263	Cys Ser Leu Gly Gly Pro Met Thr Leu Leu Pro Gly Arg Ser Asp Leu			
264	820	825	830	2601
266	tct ggg gtg gac gtc act atg ctg aac atg ctc aac aga agg gac agc			
267	Ser Gly Val Asp Val Thr Met Leu Asn Met Leu Asn Arg Arg Asp Ser			
268	835	840	845	

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270	agc gcc agc acc atc agc tcg gcc tac ctg agc agc cgc cgc tcc tca	2649
271	Ser Ala Ser Thr Ile Ser Ser Ala Tyr Leu Ser Ser Arg Arg Ser Ser	
272	850 855 860 865	
274	ggg atc tcg ccc tgc ttc tcc agc cgc cgc tcc agc gag gcg tca cag	2697
275	Gly Ile Ser Pro Cys Phe Ser Ser Arg Arg Ser Ser Glu Ala Ser Gln	
276	870 875 880	
278	gcc gag ggc cgg ccg cag aac gtg agc gtg gcc gac tcc tac gac ccc	2745
279	Ala Glu Gly Arg Pro Gln Asn Val Ser Val Ala Asp Ser Tyr Asp Pro	
280	885 890 895	
282	atc tcc acc gac gcc tcg cgc cgc tcc agc gaa gcc agc cag agc gac	2793
283	Ile Ser Thr Asp Ala Ser Arg Arg Ser Ser Glu Ala Ser Gln Ser Asp	
284	900 905 910	
286	ggc ctg ccc agc ctg ctc agc ctc acg ccc gcc cag cag tac cgc ctc	2841
287	Gly Leu Pro Ser Leu Leu Ser Leu Thr Pro Ala Gln Gln Tyr Arg Leu	
288	915 920 925	
290	aag gcc aag tac gcg gct gcc aca gga ggg ccg ccg ccg acg .ccc ctg	2889
291	Lys Ala Lys Tyr Ala Ala Ala Thr Gly Gly Pro Pro Pro Thr Pro Leu	
292	930 935 940 945	
294	ccc aac atg gag agg atg agc ctg aag acg cgc ctg gcg ctg ctc ggg	2937
295	Pro Asn Met Glu Arg Met Ser Leu Lys Thr Arg Leu Ala Leu Leu Gly	
296	950 955 960	
298	gat gcc ctc gag cct ggc gtg gcc ctg cct cca gtt cat gcc ccg agg	2985
299	Asp Ala Leu Glu Pro Gly Val Ala Leu Pro Pro Val His Ala Pro Arg	
300	965 970 975	
302	agg tgc agc gac ggg gga gcc cac ggc tac ggg ccg cgc cac ctg cag	3033
303	Arg Cys Ser Asp Gly Gly Ala His Gly Tyr Gly Arg Arg His Leu Gln	
304	980 985 990	
306	ccg cac gat gcg ctg ggc cac ggc gtg agg agg gcc agc gac ccg gtg	3081
307	Pro His Asp Ala Leu Gly His Gly Val Arg Arg Ala Ser Asp Pro Val	
308	995 1000 1005	
310	cgg aca ggc tcc gag ggc ctg gcc ctg cct cgt gtg ccg cgc ttc agc	3129
311	Arg Thr Gly Ser Glu Gly Leu Ala Leu Pro Arg Val Pro Arg Phe Ser	
312	1010 1015 1020 1025	
314	agc ctc agc agc tgc aac ccc ccg gcg atg gcc acg tcc gcg gag aag	3177
315	Ser Leu Ser Ser Cys Asn Pro Pro Ala Met Ala Thr Ser Ala Glu Lys	
316	1030 1035 1040	
318	cgc agt ctc gtg ctt cag aat tac acg ccg ccc gag ggc ggc cag tcc	3225
319	Arg Ser Leu Val Leu Gln Asn Tyr Thr Arg Pro Glu Gly Gly Gln Ser	
320	1045 1050 1055	
322	cga aac ttc cac tcg tcc ccc tgt cct ccc agc atc acc gag aac gtc	3273
323	Arg Asn Phe His Ser Ser Pro Cys Pro Pro Ser Ile Thr Glu Asn Val	
324	1060 1065 1070	
326	acc ctg gag tcc ctg acc atg gac gct gat gcc aac ctg aac gat gag	3321
327	Thr Leu Glu Ser Leu Thr Met Asp Ala Asp Ala Asn Leu Asn Asp Glu	
328	1075 1080 1085	
330	gat ttc ctg ccg gac gac gtg gtg cag tat tta aat tcc cag aac caa	3369
331	Asp Phe Leu Pro Asp Asp Val Val Gln Tyr Leu Asn Ser Gln Asn Gln	
332	1090 1095 1100 1105	
334	gca ggg tac gag cag cac ttc ccc agc gcc ctc ccg gac gac agc aaa	3417

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date